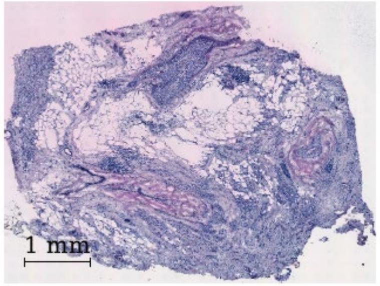
Computer vision AI to characterize human health and disease

James Zou

Stanford University

Chan-Zuckerberg Investigator

(video removed)



What do you see?

69 years old man

Left face sagging

White silver hair

Deep wrinkles

Elongated face

Bytes of information

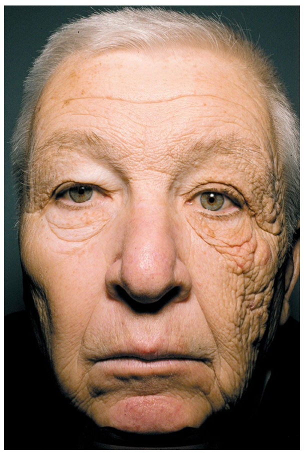
Gordon J et al. **NEJM** 2012

What do you see?

Gordon J et al. **NEJM** 2012

MBs of information

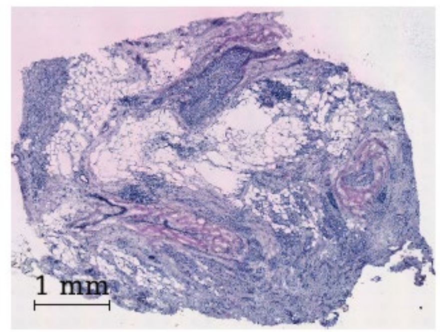
Information is visual



Heart ultrasound

(video removed)

Tumor biopsy



Microglia

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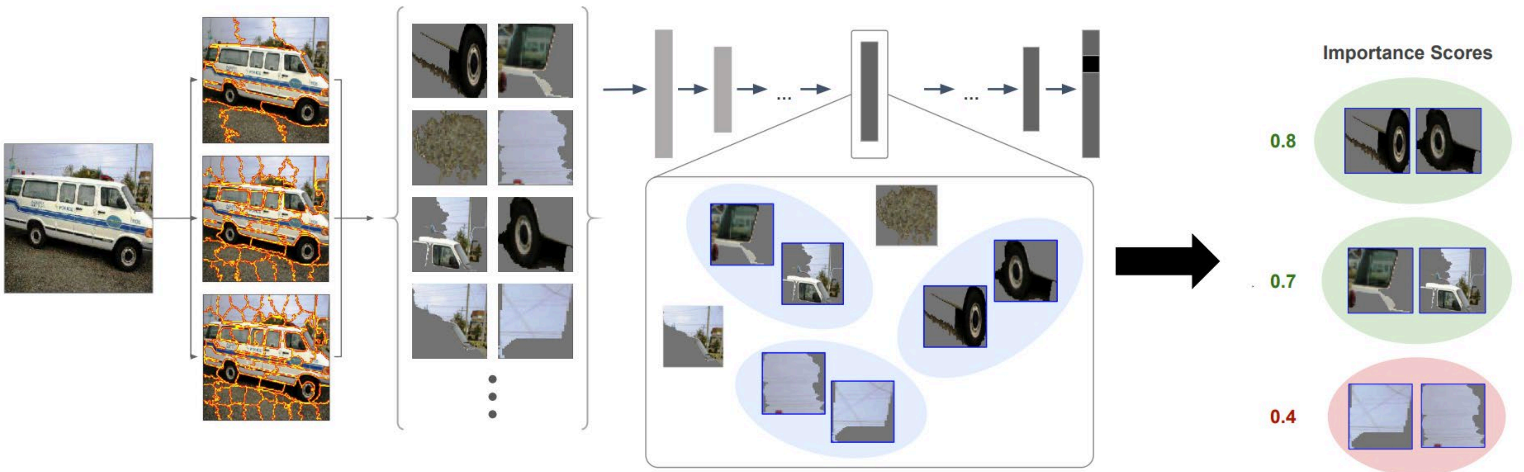
How would you describe these?

Goal: comp. vision → new language of morphology and biology/disease

Computer vision advances

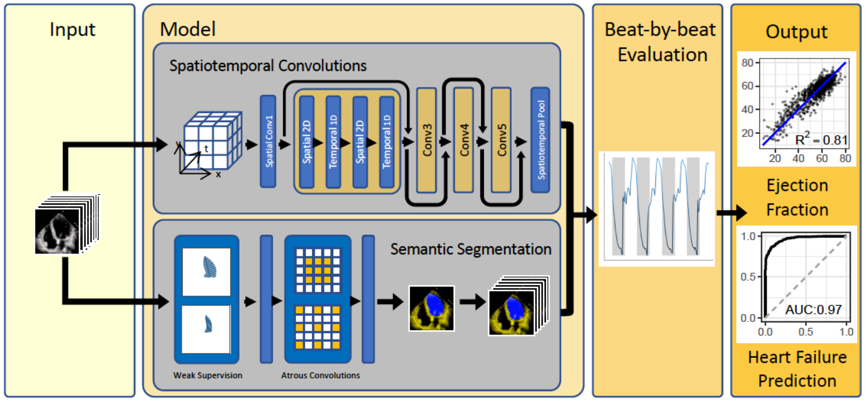
(video removed)



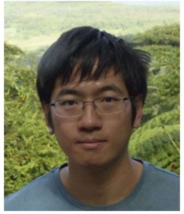
Ghorbani, Wexler, Zou, Kim *NeurIPS* 2019

Vision for heart

(video removed)



Video AI for assessing cardiac function. *Nature* 2020.
Ouyang, He, Ghorbani, Yuan, Ebinger, Langlotz, Heidenreich, Harrington, Liang, Ashley, Zou



Vision for heart

Heart disease is the leading cause of death in the US.
1in 4 death (>600k/year)

(video removed)

Function score
(ejection fraction)

Echocardiogram is routinely used to assess heart function.
>10 million/year in the US. Each one costs >$1000.

Human vision is the driver of cardiac assessment

Heart disease is the leading cause of death in the US.
1in 4 death (>600k/year)

(video removed)

Human vision is expensive, time-consuming and variable.

Computer vision can be faster and more reliable

Algorithm output

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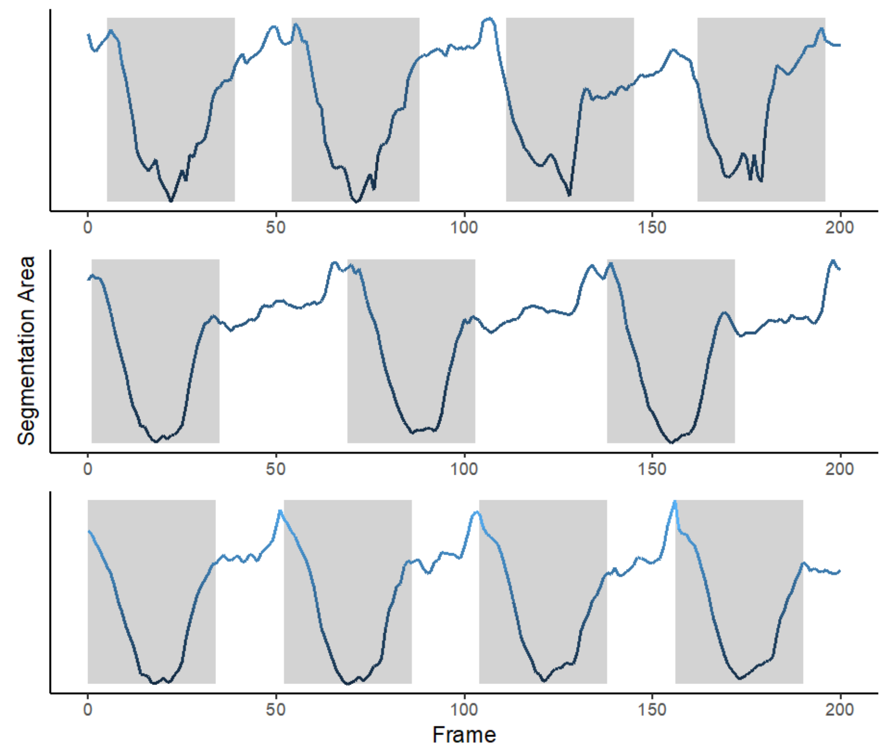
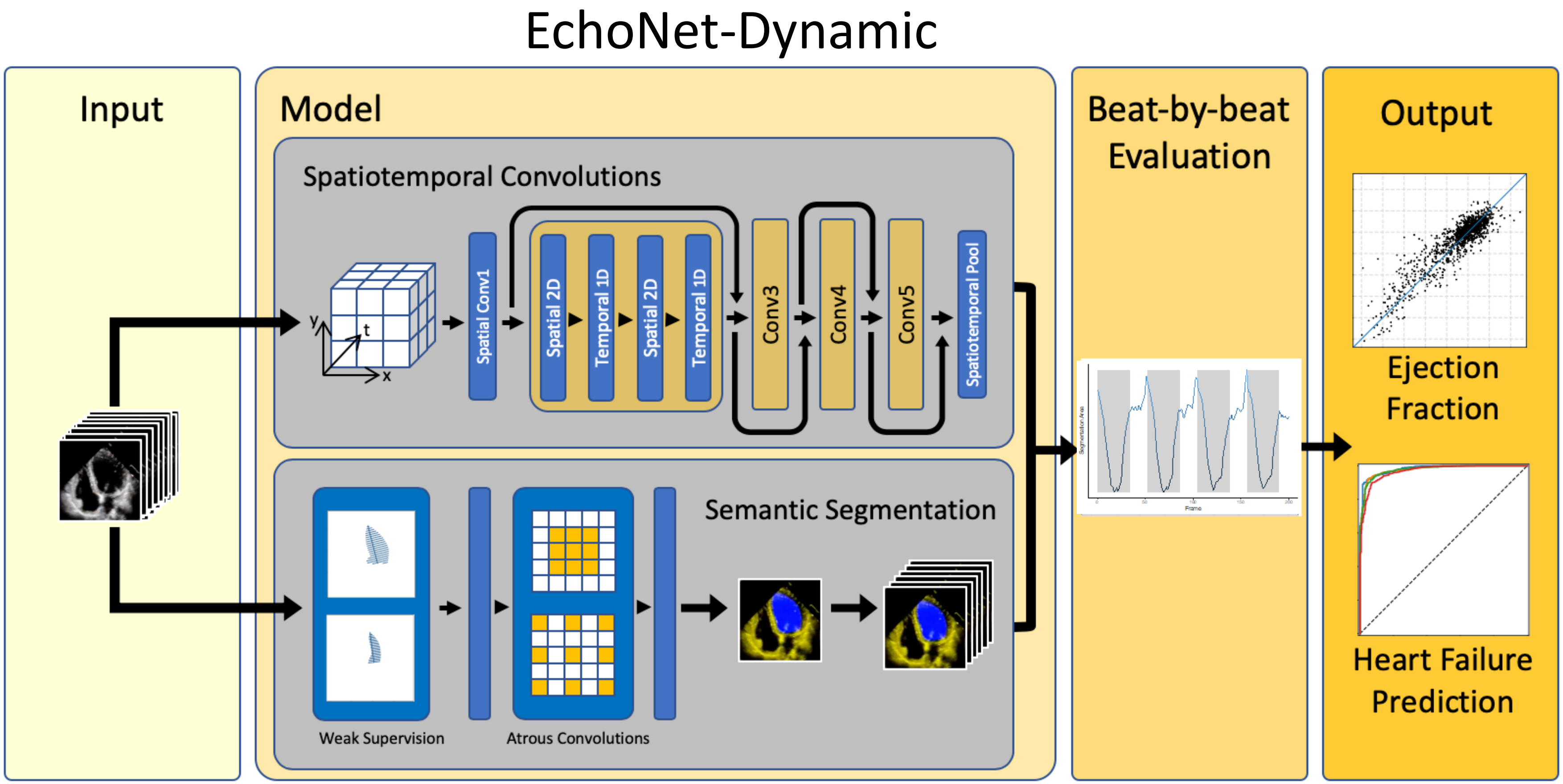
EchoNet assessed chamber area



Ouyang et al. *Nature* 2020

Algorithm mimics clinical workflow



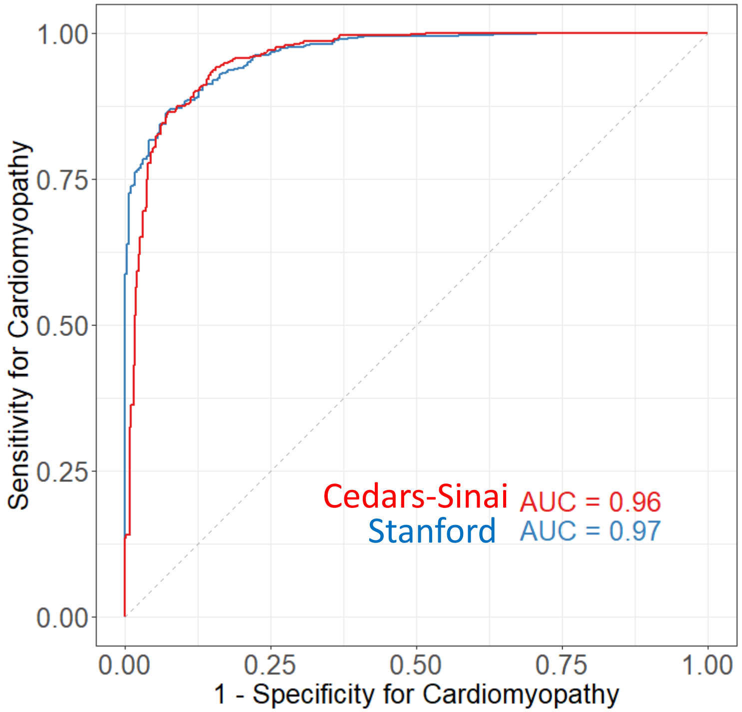
Kidney
Liver
…

Idea: use temporal segmentation to focus attention of model.

Ouyang et al. *Nature* 2020

Achieves expert performance in new hospital

Predicting heart failure



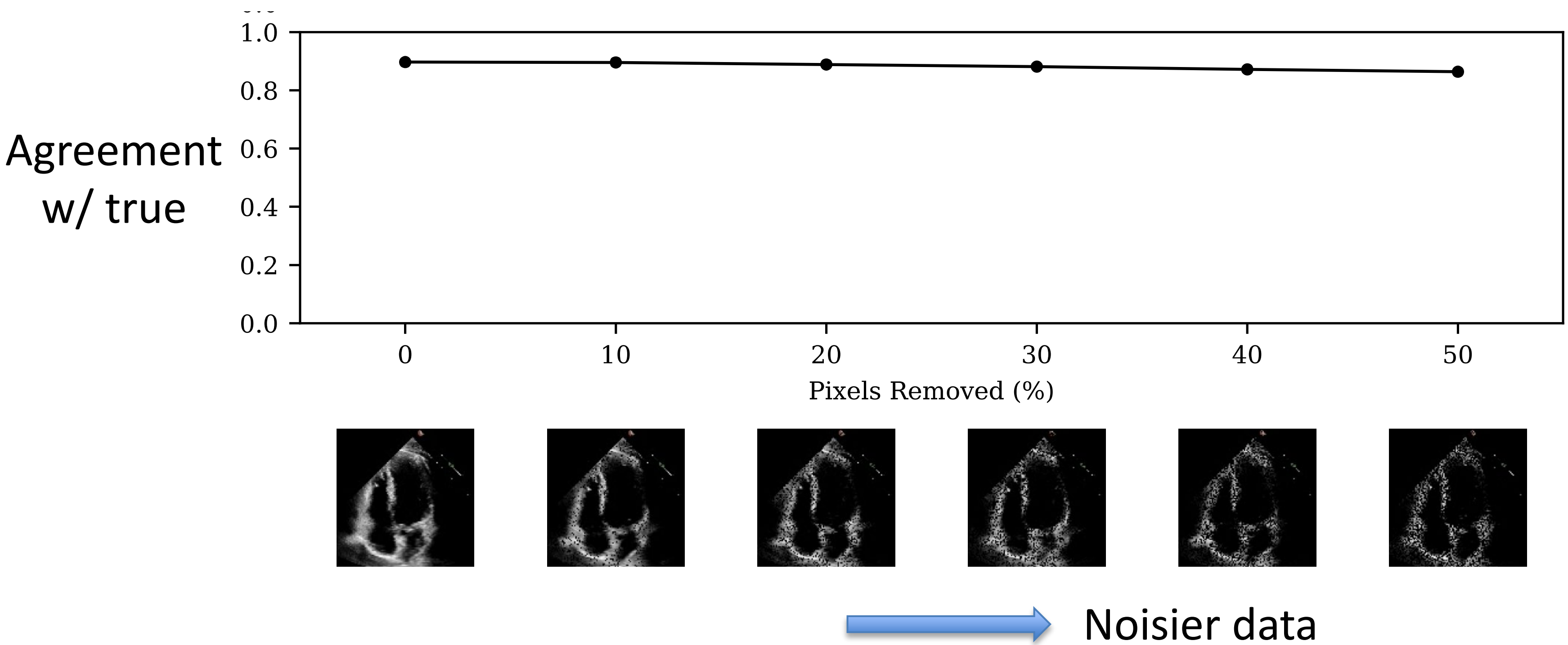
Examples

(video removed)

Ouyang et al. *Nature* 2020

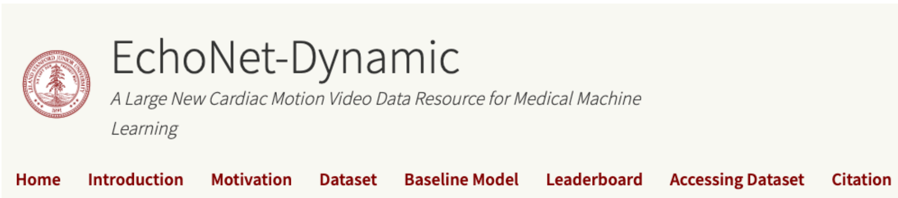
Algorithm robust to noisy videos

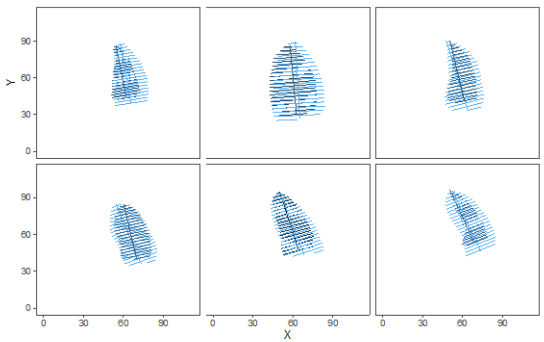
Maintains good performance when 50% of video is corrupted



Ouyang et al. *Nature* 2020

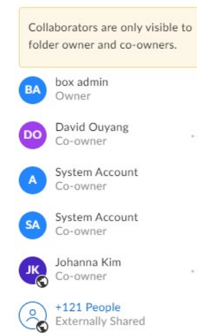
Open dataset and code

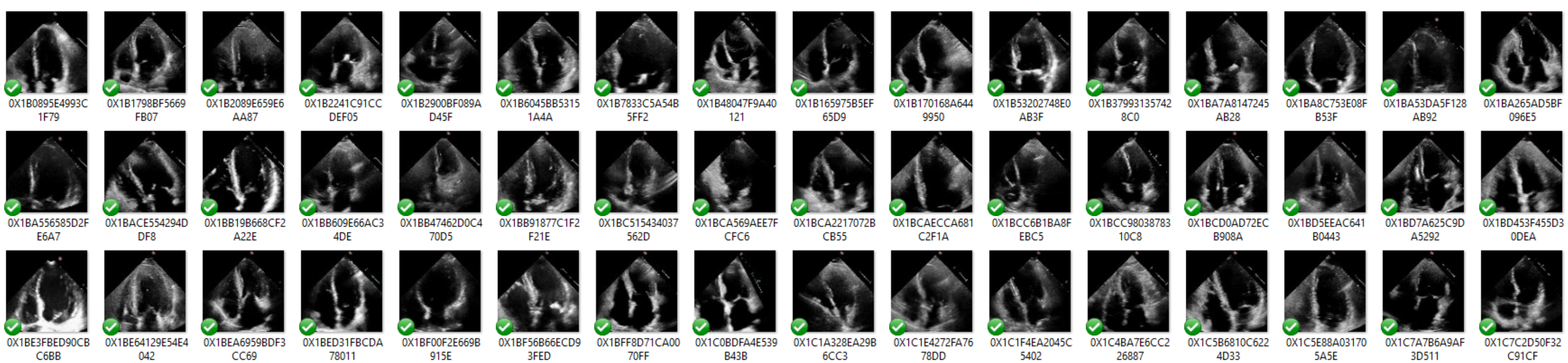




Dataset Label Variables

Variable	Description
FileName	Hashed file name used to link videos, labels, and annotations
EF	Ejection fraction calculated from ESV and EDV
ESV	End systolic volume calculated by method of discs
EDV	End diastolic volume calculated by method of discs
Height	Video Height
Width	Video Width
FPS	Frames Per Second
NumFrames	Number of Frames in whole video
Split	Classification of train/validation/test sets used for benchmarking



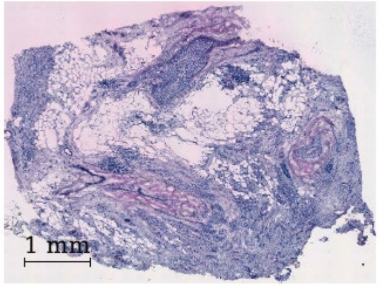


Largest public dataset of medical videos.

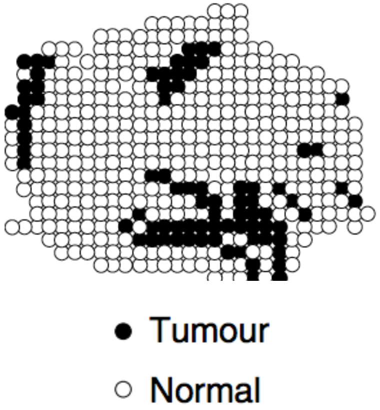
Ouyang et al. *Nature* 2020

Vision for histopathology

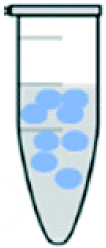
Histology image (breast cancer)



Clinician annotation



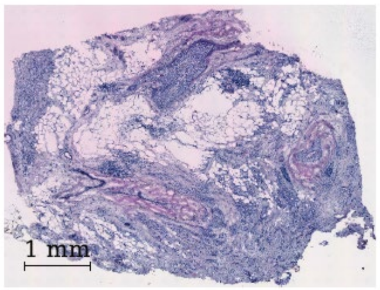
Single cell analysis loses spatial information



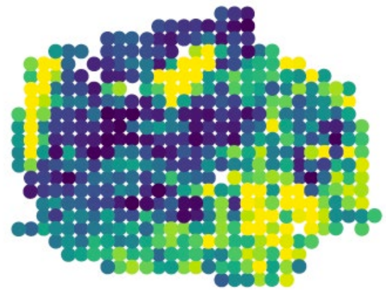
ST-Net: histology to spatial genomics

ST-Net generated expression

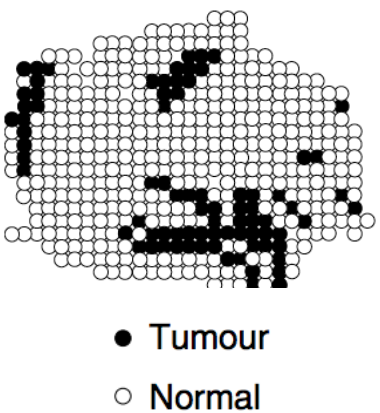
Histology image



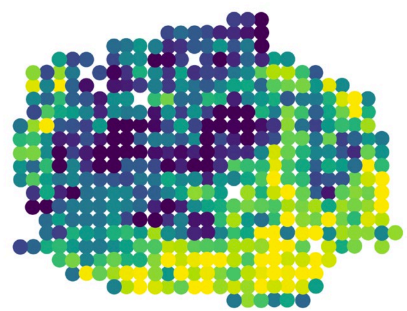
FASN



Clinician annotation

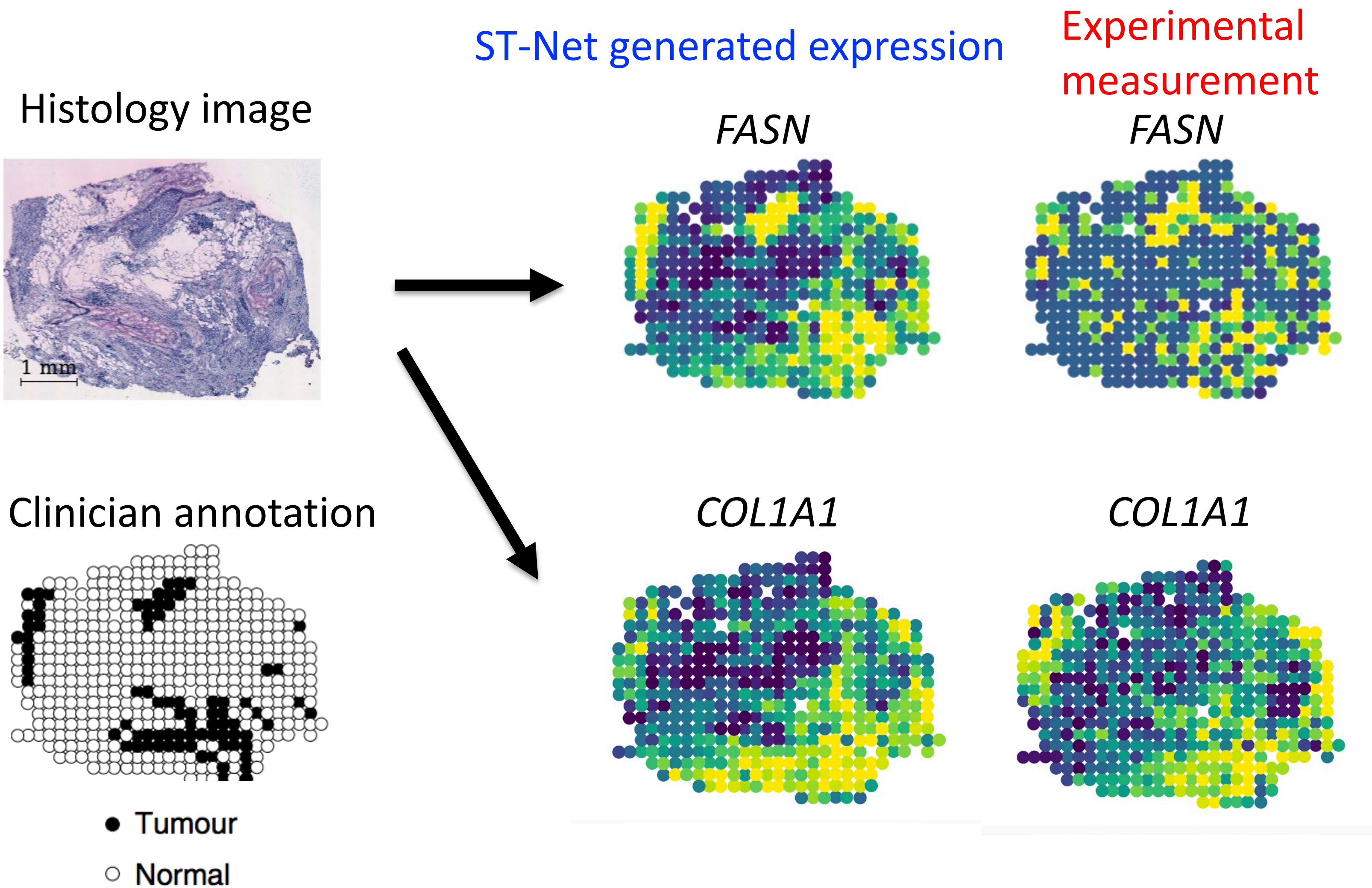


COL1A1



Accurately generates spatial expression of >100 genes.

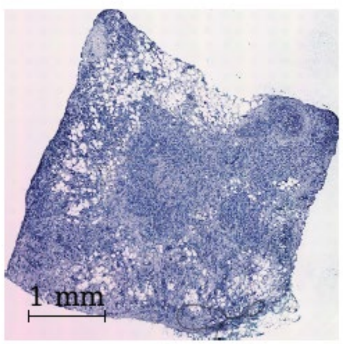
ST-Net: histology to spatial genomics



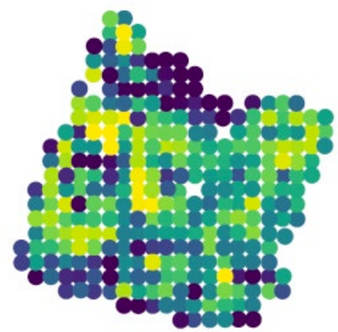
Accurately generates spatial expression of >100 genes.

Works well across patients

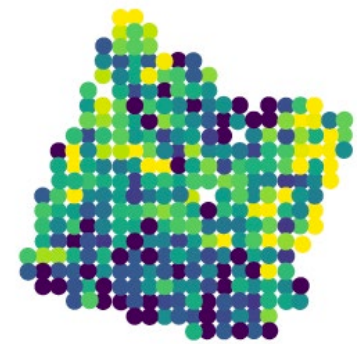
Histology image



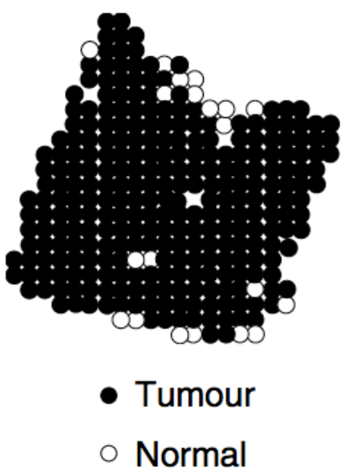
ST-Net generated FASN expression



Experimental FASN measurement



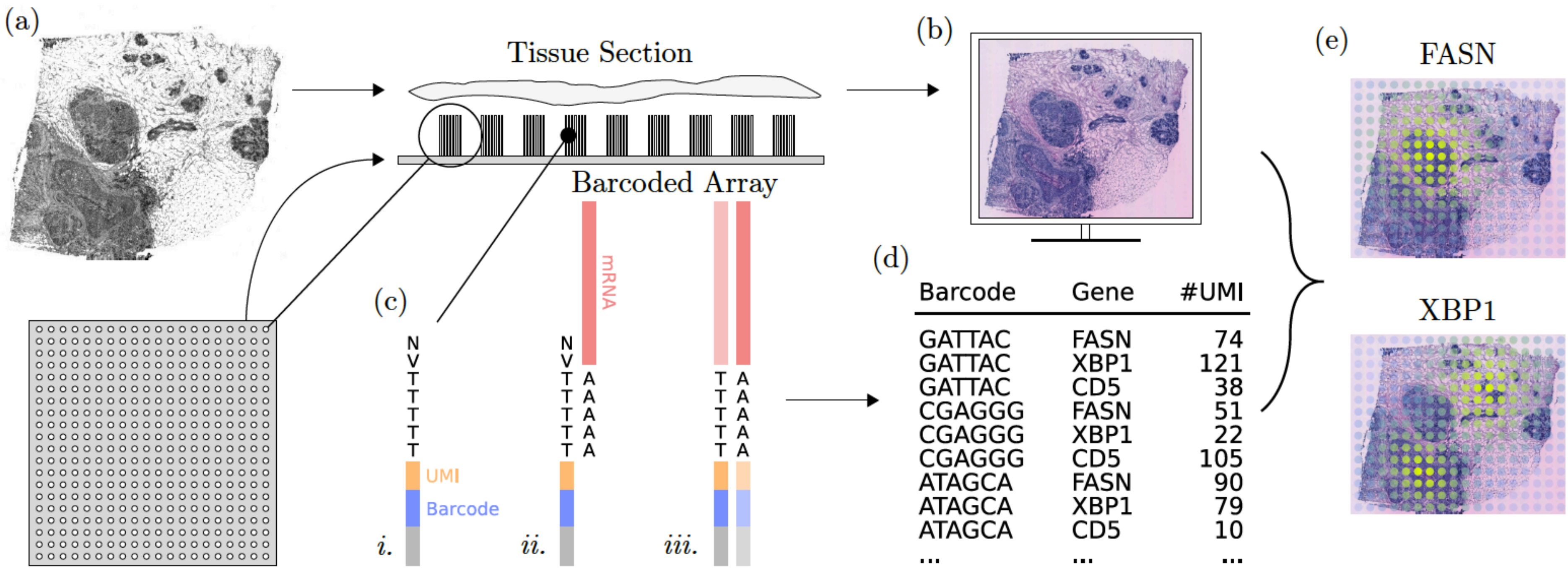
Clinician annotation



Paper:
He, Bergenstrahle, Stenbeck, Abid, Andersson, Borg, Maaskola, Lundeberg, Zou. Nature Biomedical Eng. (2020)

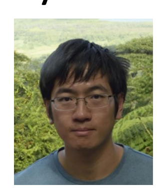
Spatial transcriptomics technology

Spatial transcriptomics measurements of hundreds of genes in breast tumor



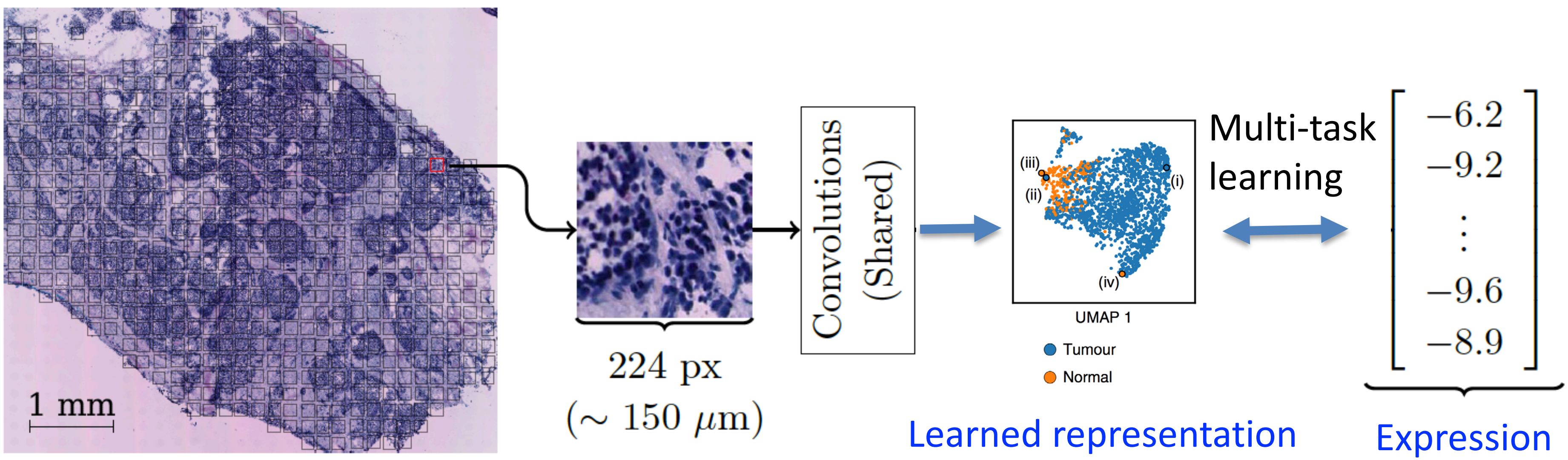
Each probe is ~100 microns

Bryan He



Joakim Lundeberg

ST-Net: image to transcriptome profile translation

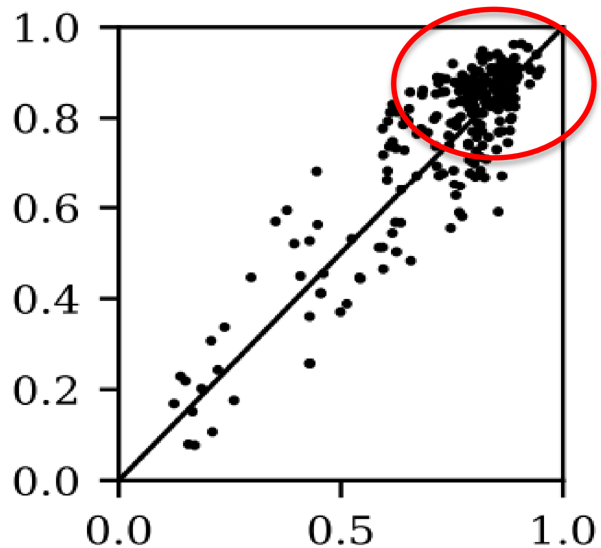


ST-Net accurately imputes >100 genes at 100 micron resolution.
Trained on over >30k spatially resolved transcriptomes.

He et al. *Nature BME* 2020

Validated on external patient samples

AUC on test 2



AUC on test set 1

100 genes that we can generate accurate spatial profile:

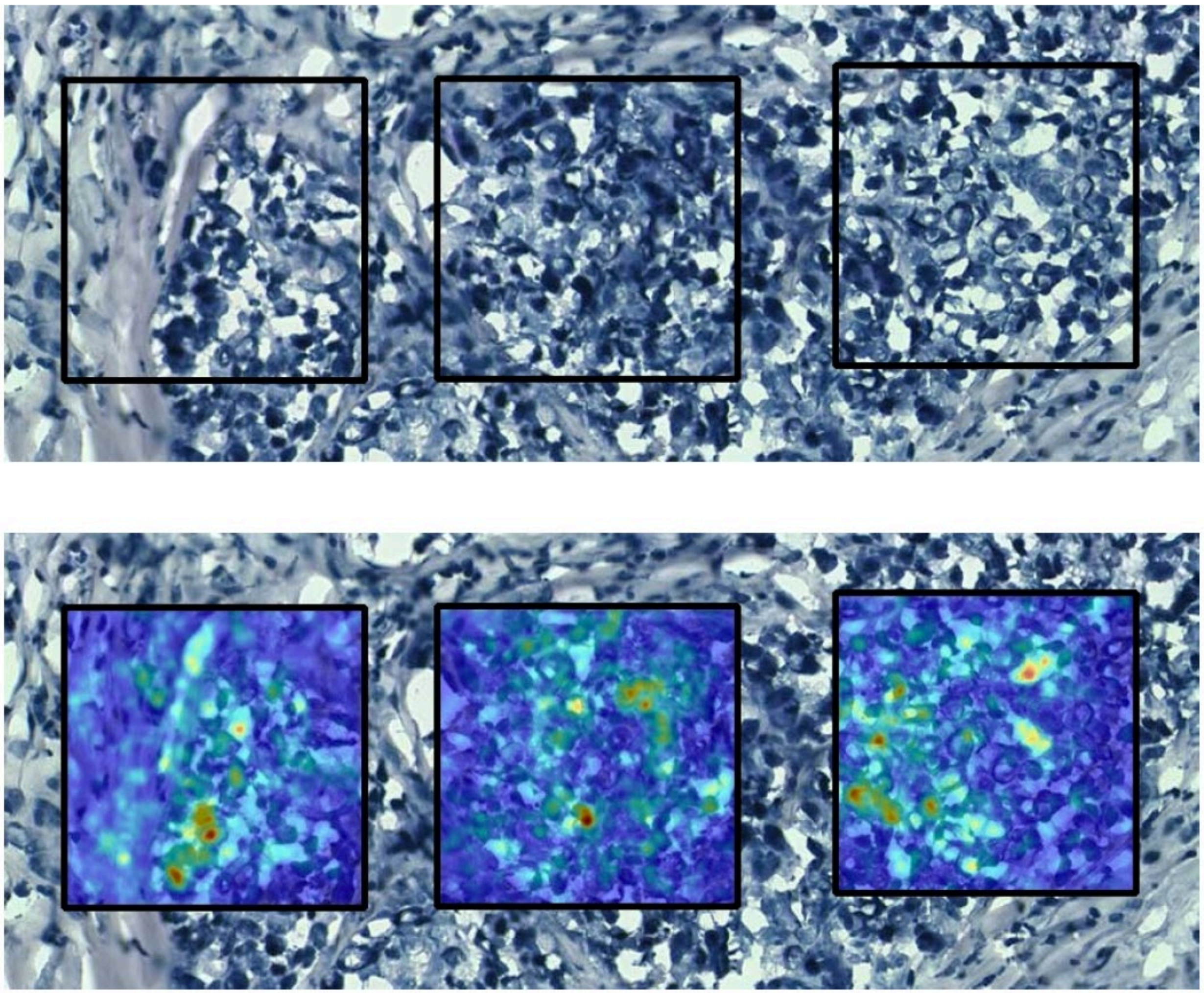
- tumor makers
- immune markers
- mobility and architecture genes

Each dot = one gene.

He et al. *Nature BME* 2020

ST-Net maps sub-cellular morphology to expression

Input image



Computational prediction of where *FASN* is expressed

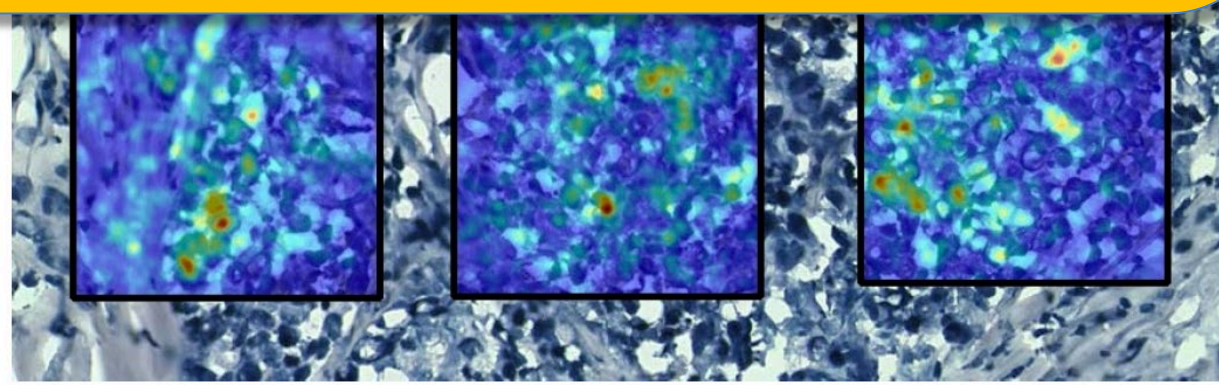
He et al. *Nature BME* 2020

Expression ↔ morphology association

Association betw expression of each gene to morphology

	Nucleus size (pixels^2)	Axis Ratio	Nuclear Density
GNAS	0.21 ($p = 5 \times 10^{-4}$)	-0.25 ($p = 6 \times 10^{-6}$)	0.26 ($p = 3 \times 10^{-3}$)
ACTG1	0.25 ($p = 5 \times 10^{-4}$)	-0.23 ($p = 5 \times 10^{-4}$)	0.14 ($p = 2 \times 10^{-1}$)
FASN	0.25 ($p = 5 \times 10^{-4}$)	-0.23 ($p = 6 \times 10^{-6}$)	0.00 ($p = 4 \times 10^{-2}$)
DDX5	0.27 ($p = 7 \times 10^{-5}$)	-0.25 ($p = 6 \times 10^{-6}$)	0.23 ($p = 1 \times 10^{-2}$)
XBP1	0.18 ($p = 5 \times 10^{-4}$)	-0.17 ($p = 5 \times 10^{-4}$)	0.12 ($p = 1 \times 10^{-2}$)

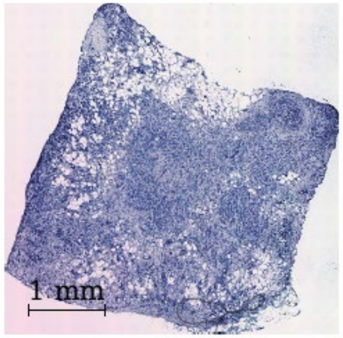
+ 100 other genes

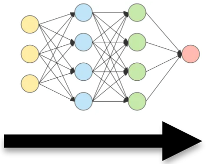


He et al. *Nature BME* 2020

Works well on previously collected images

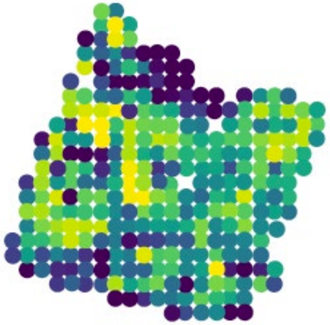
Any histology image





ST-Net

Computationally synthesized FASN expression

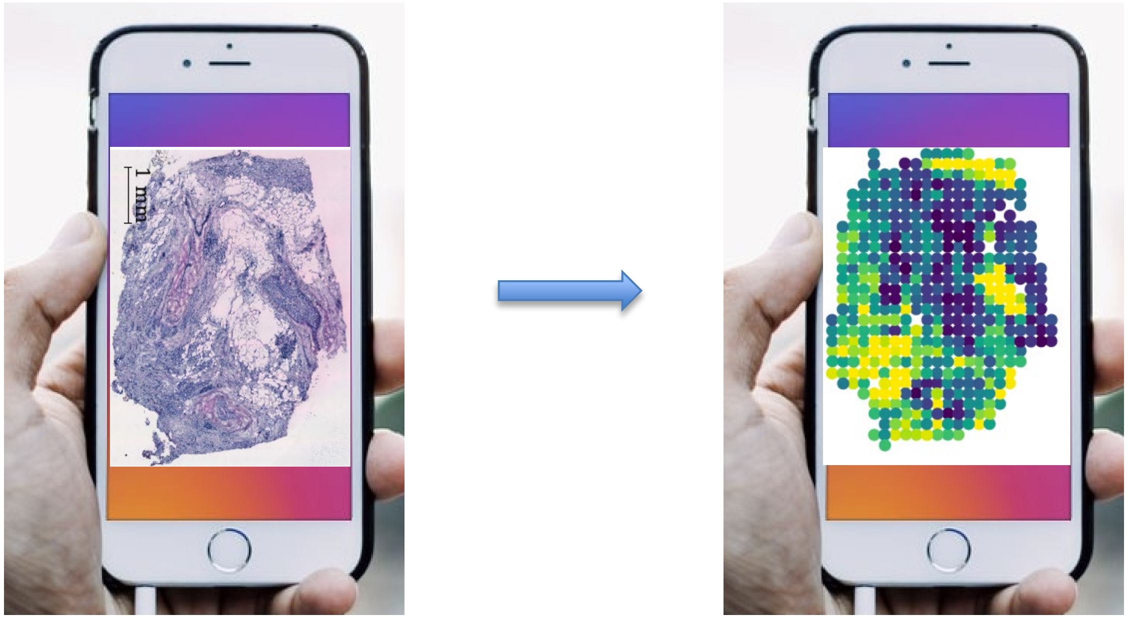


Can apply to archival images, e.g. from clinical labs.

Quantifies tumor heterogeneity and immune infiltration

He et al. *Nature BME* 2020

Applications



Insta-pathology: real-time generation of spatial genomics profiles.

Prognosis + treatment design using tumor heterogeneity.

Cell biology: linking genes to cellular morphology

Resources

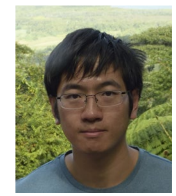
Papers and codes available www.james-zou.com

Video-based AI for cardiac assessment.

Ouyang et al. *Nature* 2020

Deep learning for generating spatial transcriptomics.

He et al. *Nature Biomedical Engineering* 2020



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